IN THE CLAIMS

Please substitute the following claim set for those currently of record:

1. -36. (Cancelled)

37. (Currently amended) ~~The method of claim 36~~ A method for analyzing nucleotide sequence variations, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to product beads;

determining a sequence feature of the one species of analyte DNA molecule which is bound to the product beads;

~~wherein the step of~~ isolating ~~is performed~~ using fluorescence activated cell sorting product beads which are bound to a plurality of copies of a first species of analyte DNA molecule from product beads which are bound to a plurality of copies of a second species of analyte DNA molecule.

38. (Cancelled)

39. (Currently amended) ~~The method of claim 36~~ A method for analyzing nucleotide sequence variations, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to

product beads;

determining a sequence feature of the one species of analyte DNA molecule which is bound to the product beads;

isolating product beads which are bound to a plurality of copies of a first species of analyte DNA molecule from product beads which are bound to a plurality of copies of a second species of analyte DNA molecule;

~~further comprising the step of~~ amplifying the first species of analyte DNA molecule from the isolated product beads.

40. (Cancelled)

41. (Cancelled)

42. (Cancelled)

43. (Currently amended) ~~The method of claim 35~~ A method for analyzing nucleotide sequence variations, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to product beads;

determining a sequence feature of the one species of analyte DNA molecule which is bound to the product beads, ~~wherein the step of determining is performed~~ by hybridization to oligonucleotide probes which are differentially labeled.

44. (Currently amended) ~~The method of claim 35~~ A method for analyzing nucleotide sequence variations, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a

primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to product beads;

~~wherein the~~ determining relative or absolute amounts of product beads comprising one or more sequence features ~~is determined~~.

45. (Original) The method of claim 44 wherein the relative or absolute amounts are determined using flow cytometry.

46. -59. (Cancelled)

60. (Currently amended) ~~The method of claim 59 wherein the step of isolating is performed~~ A method for isolating nucleotide sequence variants, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a primer for amplifying the analyte DNA molecules, whereby product beads are formed which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to product beads;

isolating using fluorescence activated cell sorting product beads which are bound to a plurality of copies of a first species of analyte DNA molecule from product beads which are bound to a plurality of copies of a second species of analyte DNA molecule.

61. (Cancelled)

62. (Currently amended) ~~The method of claim 59 further comprising the step of~~ A method for isolating nucleotide sequence variants, comprising:

forming microemulsions comprising one or more species of analyte DNA molecules;

amplifying analyte DNA molecules in the microemulsions in the presence of reagent beads, wherein the reagent beads are bound to a plurality of molecules of a primer for amplifying the analyte DNA molecules, whereby product beads are formed

which are bound to a plurality of copies of one species of analyte DNA molecule;

separating the product beads from analyte DNA molecules which are not bound to product beads;

isolating product beads which are bound to a plurality of copies of a first species of analyte DNA molecule from product beads which are bound to a plurality of copies of a second species of analyte DNA molecule;

amplifying the first species of analyte DNA molecule from the isolated product beads.

63. -84. (Cancelled)